

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/551,977A
Source: 1Fw16
Date Processed by STIC: 7/18/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u> | <u>SUGGESTED CORRECTION</u> | SERIAL NUMBER: <u>10/551,977A</u> |
|--|--|-----------------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 _____ Wrapped Nucleics Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." | |
| 2 _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 <u> </u> Misaligned Amino Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. | |
| 4 _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 _____ PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 7 _____ Skipped Sequences (OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 _____ Skipped Sequences (NEW RULES) | Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 9 _____ Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. | |
| 10 _____ Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below) | |
| 11 _____ Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules | |
| 12 _____ PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 _____ Misuse of n/Xaa | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid | |



IFW16

RAW SEQUENCE LISTING

DATE: 01/18/2007

PATENT APPLICATION: US/10/551,977A

TIME: 10:42:16

Input Set : A:\SeqList.txt

Output Set: N:\CRF4\01182007\J551977A.raw

4 <110> APPLICANT: DEPERTHES, David
 5 CLOUTIER, Sylvain
 6 MACH, Jean-Pierre
 7 HOLLER, Nils
 8 FATTAH, Omar
 10 <120> TITLE OF INVENTION: PEPTABODY FOR CANCER TREATMENT
 12 <130> FILE REFERENCE: KZI-002US
 14 <140> CURRENT APPLICATION NUMBER: 10/551977A
 15 <141> CURRENT FILING DATE: 2005-10-04
 17 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/001049
 18 <151> PRIOR FILING DATE: 2004-04-05
 20 <150> PRIOR APPLICATION NUMBER: US 60/460,490
 21 <151> PRIOR FILING DATE: 2003-04-04
 23 <160> NUMBER OF SEQ ID NOS: 30
 25 <170> SOFTWARE: PatentIn version 3.1

see pp. 1-2
 Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

131 <210> SEQ ID NO: 6
 132 <211> LENGTH: 6
 133 <212> TYPE: DNA *delete - this is not a DNA sequence*
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Artificial sequence
 137 <220> FEATURE:
 138 <223> OTHER INFORMATION: Enhancer Peptide
 140 <400> SEQUENCE: 6
 141 Tyr Ser Phe Glu Asp Leu
 E--> 142 1 *5* *5* *misaligned amino acid number (see item 3 on Error summary sheet)*
 144 <210> SEQ ID NO: 7
 145 <211> LENGTH: 7
 146 <212> TYPE: PRT
 147 <213> ORGANISM: Artificial sequence
 149 <220> FEATURE:
 150 <223> OTHER INFORMATION: Enhancer Peptide
 152 <400> SEQUENCE: 7
 153 Tyr Ser Phe Glu Asp Leu Tyr
 E--> 154 1 *5* *5* *same error*
 156 <210> SEQ ID NO: 8
 157 <211> LENGTH: 8
 158 <212> TYPE: PRT
 159 <213> ORGANISM: Artificial sequence
 161 <220> FEATURE:

DATE: 01/18/2007

TIME: 10:42:16

Input Set : A:\SeqList.txt

Output Set: N:\CRF4\01182007\J551977A.raw

162 <223> OTHER INFORMATION: Enhancer Peptide

164 <400> SEQUENCE: 8

165 Tyr Ser Phe Glu Asp Leu Tyr Arg

E--> 166 1 5 56 same env

168 <210> SEQ ID NO: 9

169 <211> LENGTH: 9

170 <212> TYPE: PRT

171 <213> ORGANISM: Artificial sequence

173 <220> FEATURE:

174 <223> OTHER INFORMATION: Enhancer Peptide

176 <400> SEQUENCE: 9

177 Tyr Ser Phe Glu Asp Leu Tyr Arg Arg

E--> 178 1 5 5 ←

191 <210> SEQ ID NO: 11

192 <211> LENGTH: 25

193 <212> TYPE: PRT

194 <213> ORGANISM: Spodoptera litura

196 <400> SEQUENCE: 11

197 Glu Asn Phe Ser Gly Gly Cys Val Ala Gly Tyr Met Arg Thr Pro Asp

198 1 5 10 15

199 Gly Arg Cys Lys Pro Thr Phe Tyr Gln

E--> 200 ~~20~~ 25 20 25 ←

VERIFICATION SUMMARY

DATE: 01/18/2007

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TIME: 10:42:17

Input Set : A:\SeqList.txt

Output Set: N:\CRF4\01182007\J551977A.raw

L:102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:100
L:134 M:280 W: Numeric Identifier already exists, Type not replaced.
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:142 M:301 E: (44) No Sequence Data was Shown, SEQ ID:6
L:142 M:252 E: No. of Seq. differs, <211> LENGTH:Input:6 Found:0 SEQ:6
L:154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:178 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:200 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11